

Sequence error report

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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu May 03 16:48:36 EDT 2007

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Reviewer Comments:

<210> 4

<211> 6223

<212> DNA

<213> crt gene

<400> 4

The <213> response is invalid. Per 1.823 of Sequence Rules, the only valid <213> responses are: "Artificial Sequence," "Unknown," or the Genus/species. FYI: if this is an Artificial Sequence, then "crt gene" would be an insufficient explanation (please explain the source of the genetic material in the <223> response).

Same type of error in sequences 5-16

Application No: 10551508

Version No: 1.0

Input Set:

Output Set:

Started: 2007-05-03 16:08:57.906
Finished: 2007-05-03 16:08:58.290
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 384 ms
Total Warnings: 4
Total Errors: 0
No. of SeqIDs Defined: 18
Actual SeqID Count: 18

ErrCode	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)

SEQUENCE LISTING

<110> KIM, Young Tae
LEE, Jae Hyung

<120> Gene involved in the biosynthesis of carotenoid and marine
microorganism, paracoccus haeundaesis, producing the
carotenoid

<130> 428.1056

<140> 10551508

<141> 2007-05-03

<150> US 10/551,508

<151> 2005-09-29

<150> PCT/KR2004/000752

<151> 2003-03-31

<150> KR2003-20222

<151> 2003-03-31

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<210> 2

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> reverse primer for Paracoccus haeundaesis 16S rDNA

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 Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Phe Ile Ala
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 Arg Lys Met Ile Val Lys His Met Ala His His Arg His Thr Gly Thr
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 Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
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 Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
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170

175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
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Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
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Thr Val Gly Trp Ile Trp Ala Pro Val Leu Trp Trp Ile Ala Leu Gly
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His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr Ala Arg
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Arg Leu Tyr Gln Ala His Arg Leu His His Ala Val Glu Gly Arg Asp
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